Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:00:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231761.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6231761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:00:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,013,615
Mapped reads	3,433,921 / 85.56%
Unmapped reads	579,694 / 14.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,311 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	198,814 / 4.95%
Duplication rate	2.62%
Clipped reads	1,646,385 / 41.02%

2.2. ACGT Content

Number/percentage of A's	62,416,371 / 27.61%
Number/percentage of C's	43,864,131 / 19.4%
Number/percentage of T's	65,820,226 / 29.12%
Number/percentage of G's	53,940,118 / 23.86%
Number/percentage of N's	15,394 / 0.01%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0731

Standard Deviation	6.8216

2.4. Mapping Quality

Mean Mapping Quality	41.8

2.5. Mismatches and indels

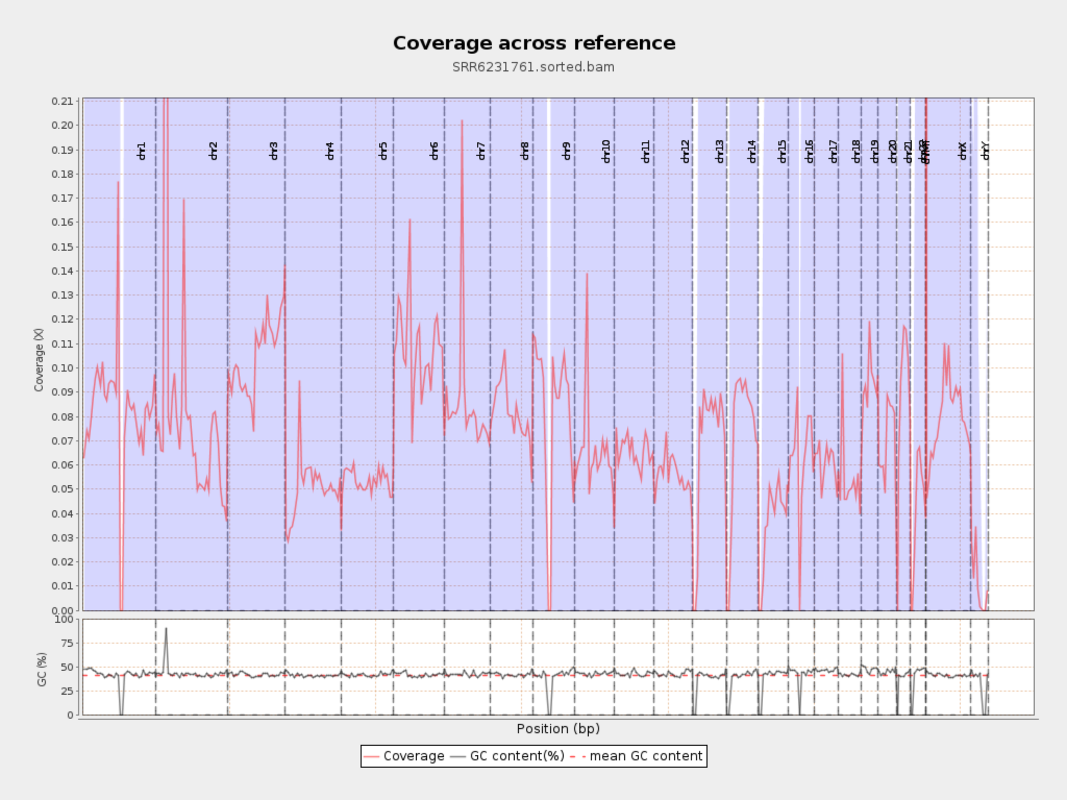
General error rate	0.69%
Mismatches	1,525,020
Insertions	17,243
Mapped reads with at least one insertion	0.5%
Deletions	58,044
Mapped reads with at least one deletion	1.67%
Homopolymer indels	44.03%

2.6. Chromosome stats

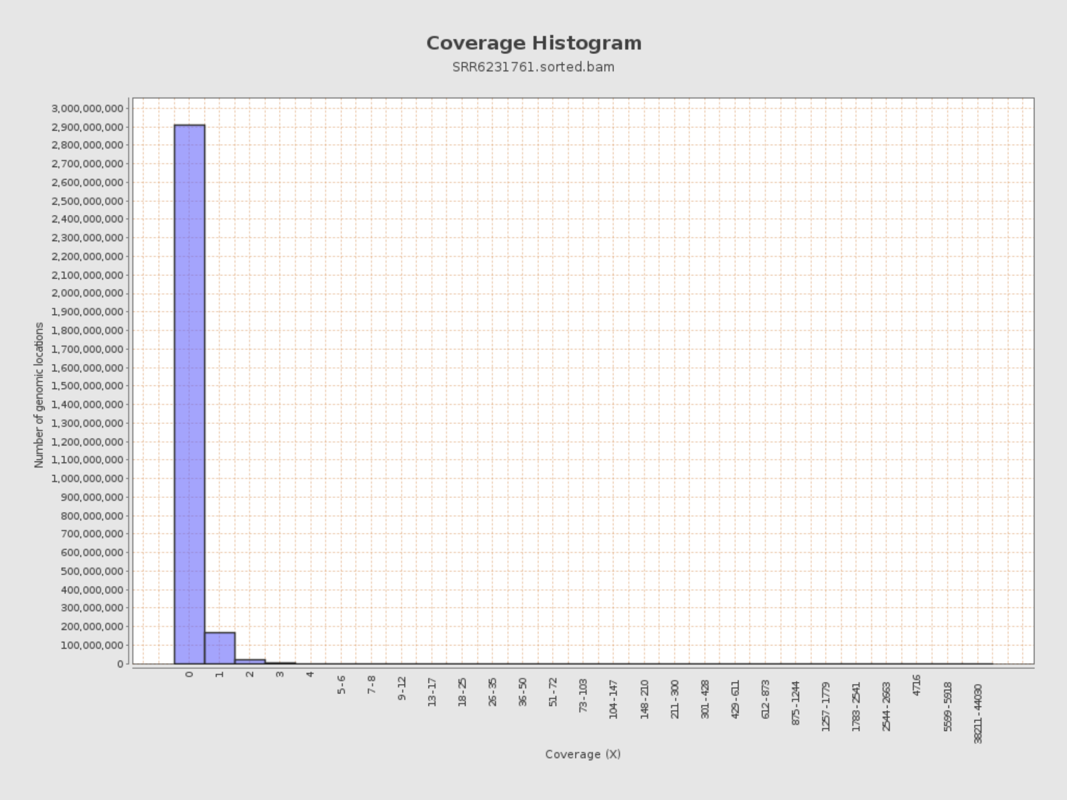
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20441032	0.082	2.0641
chr2	243199373	20922947	0.086	24.1433
chr3	198022430	20723161	0.1047	0.3726
chr4	191154276	9695440	0.0507	0.3208
chr5	180915260	9696581	0.0536	0.2834
chr6	171115067	18617271	0.1088	0.6149
chr7	159138663	13622277	0.0856	1.5227

chr8	146364022	11981050	0.0819	0.9642
chr9	141213431	11500659	0.0814	0.692
chr10	135534747	8930871	0.0659	0.7449
chr11	135006516	8810674	0.0653	0.5201
chr12	133851895	7486095	0.0559	0.2944
chr13	115169878	7862198	0.0683	0.2929
chr14	107349540	7843235	0.0731	0.4809
chr15	102531392	3648515	0.0356	0.2377
chr16	90354753	5521429	0.0611	0.4478
chr17	81195210	5000935	0.0616	0.3339
chr18	78077248	4277077	0.0548	1.5323
chr19	59128983	5546089	0.0938	1.3305
chr20	63025520	4412268	0.07	0.347
chr21	48129895	4206503	0.0874	0.3857
chr22	51304566	2105183	0.041	0.2276
chrMT	16571	273357	16.4961	9.817
chrX	155270560	12371771	0.0797	0.425
chrY	59373566	658323	0.0111	0.2225

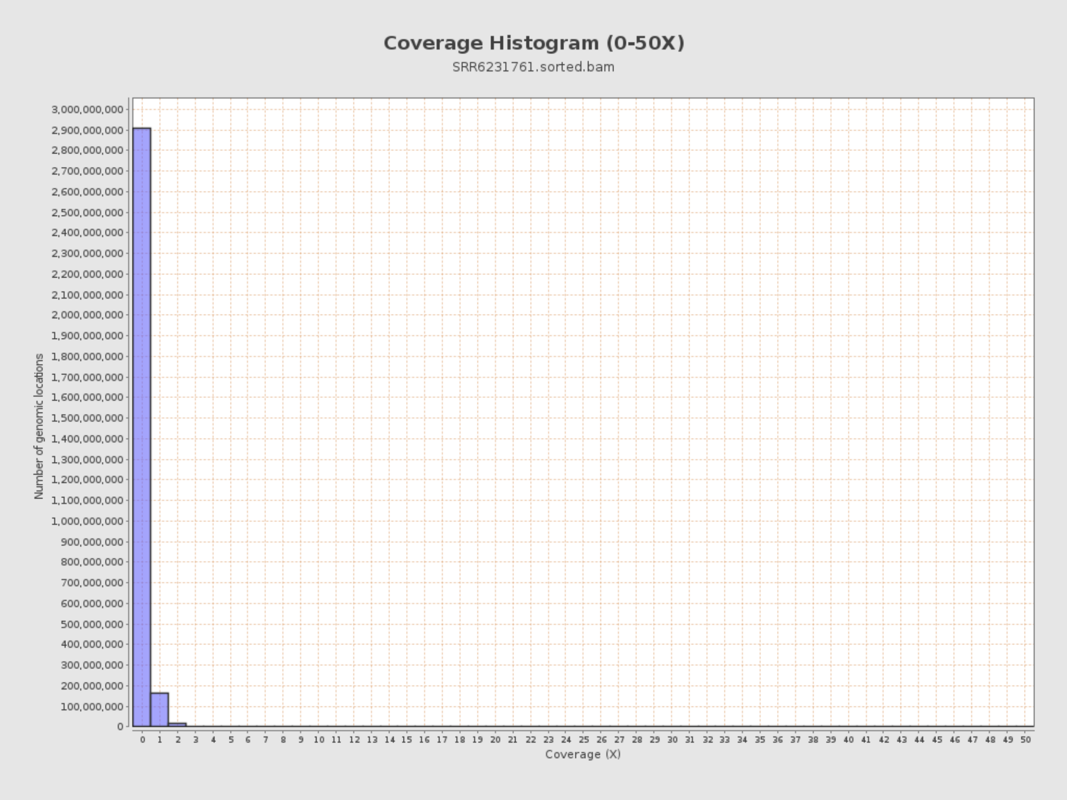
3. Results : Coverage across reference



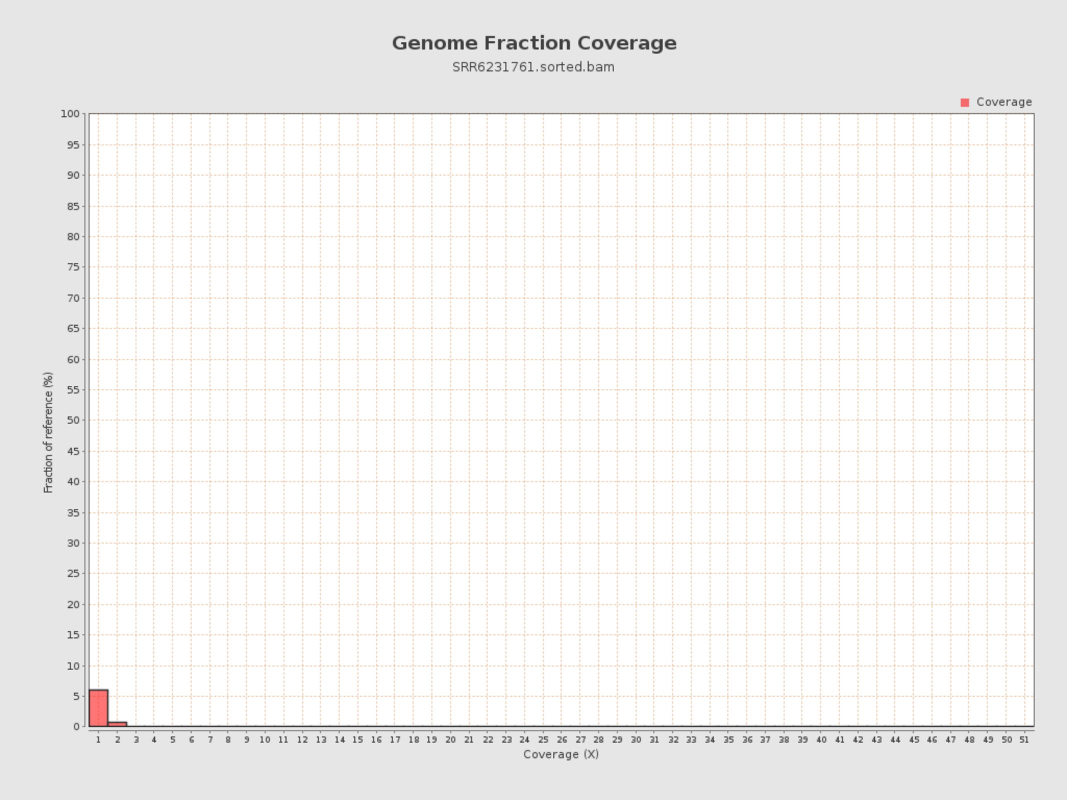
4. Results : Coverage Histogram



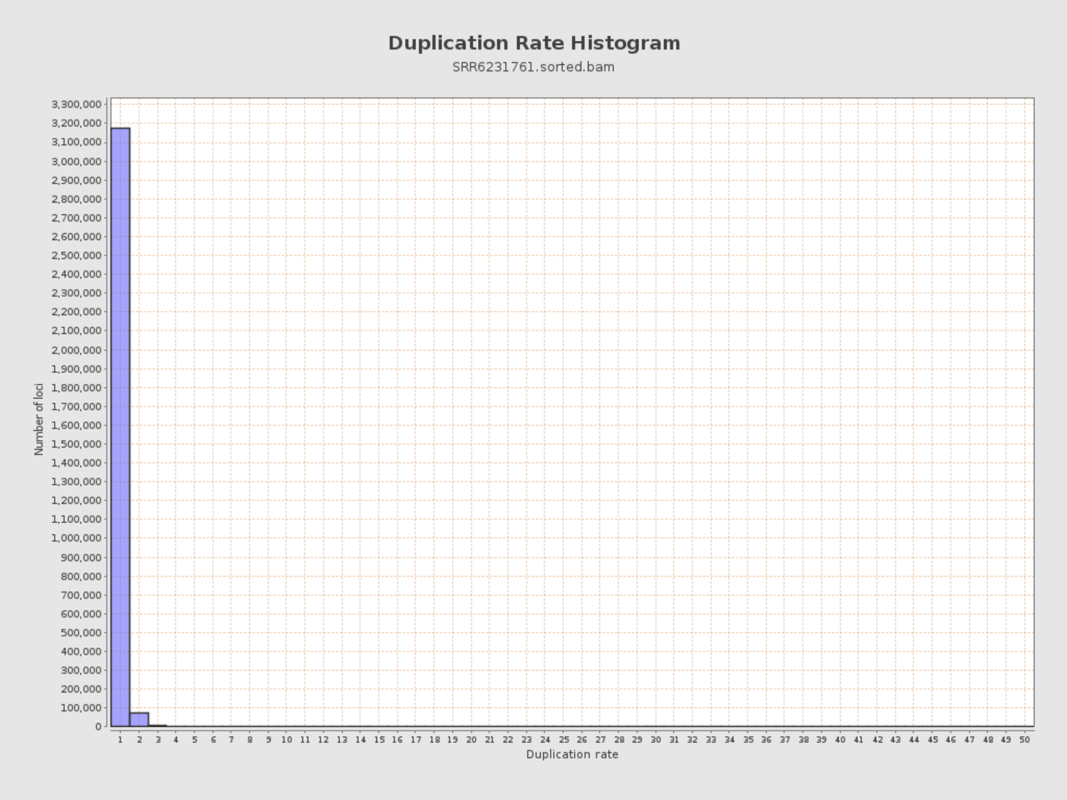
5. Results : Coverage Histogram (0-50X)



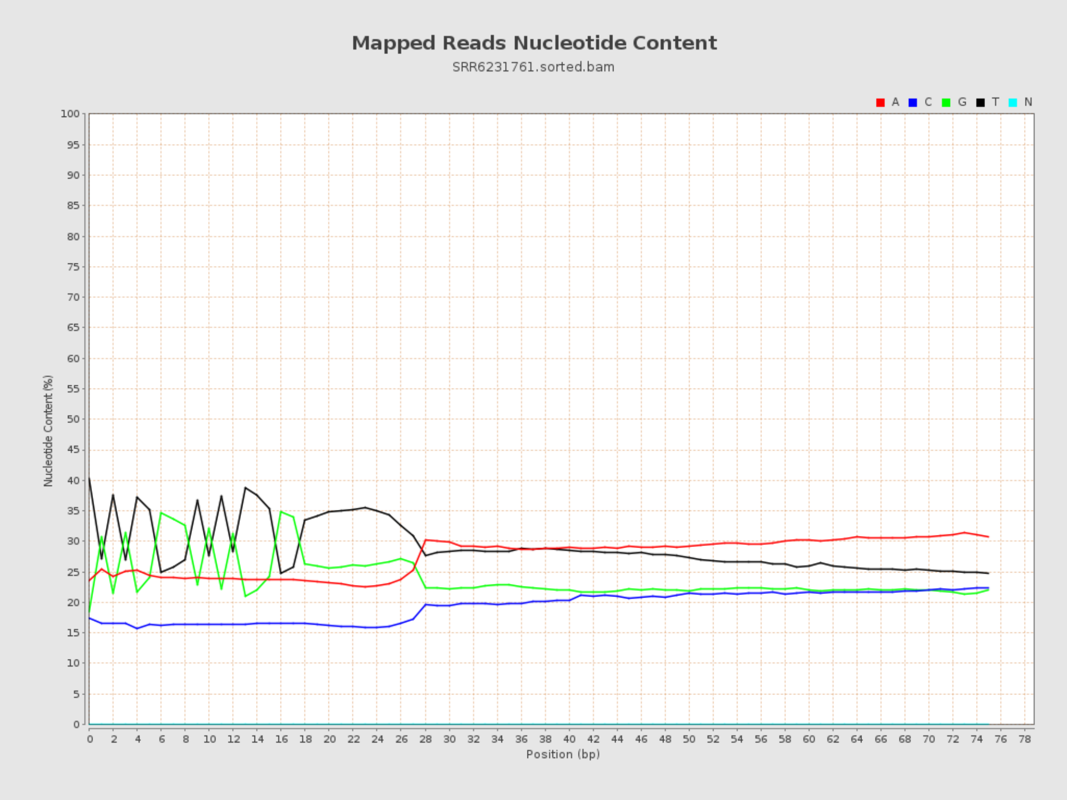
6. Results : Genome Fraction Coverage



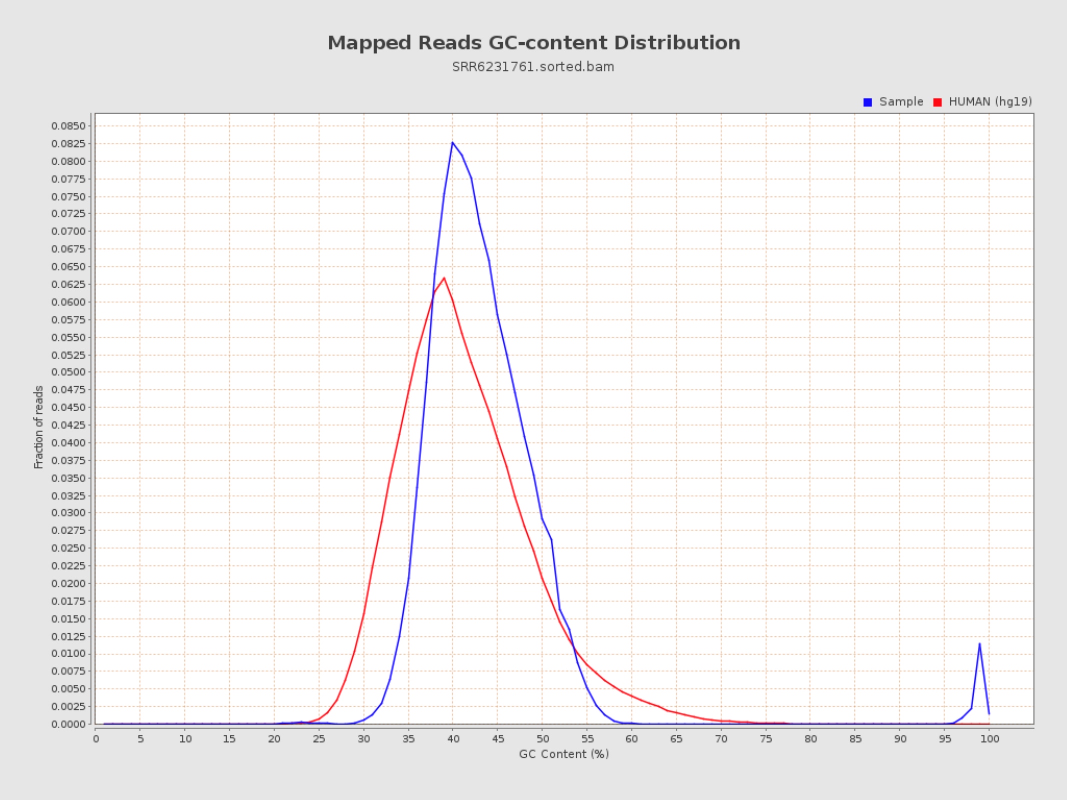
7. Results : Duplication Rate Histogram



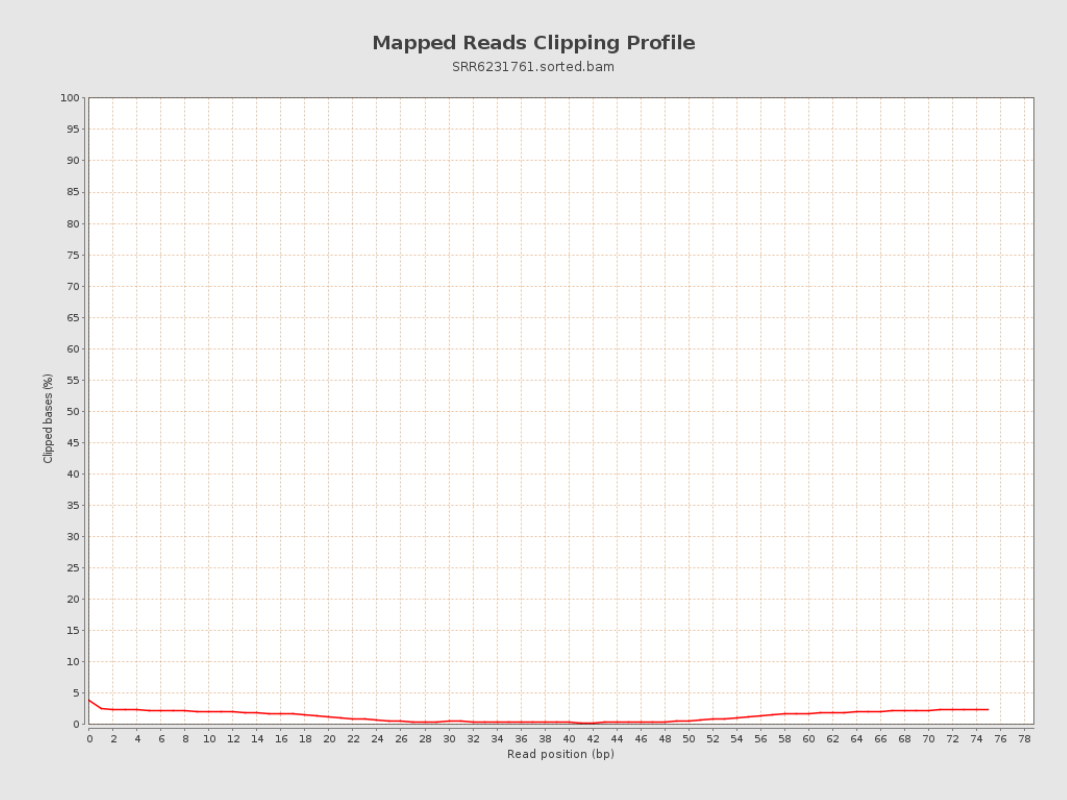
8. Results : Mapped Reads Nucleotide Content



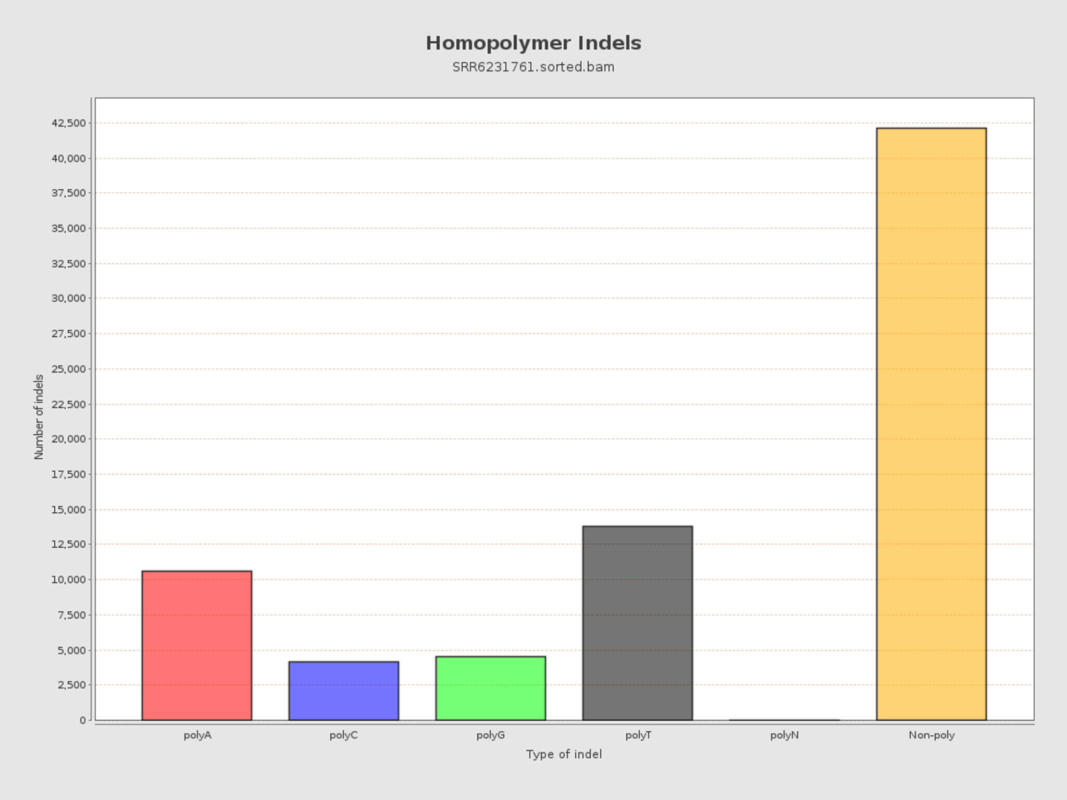
9. Results : Mapped Reads GC-content Distribution



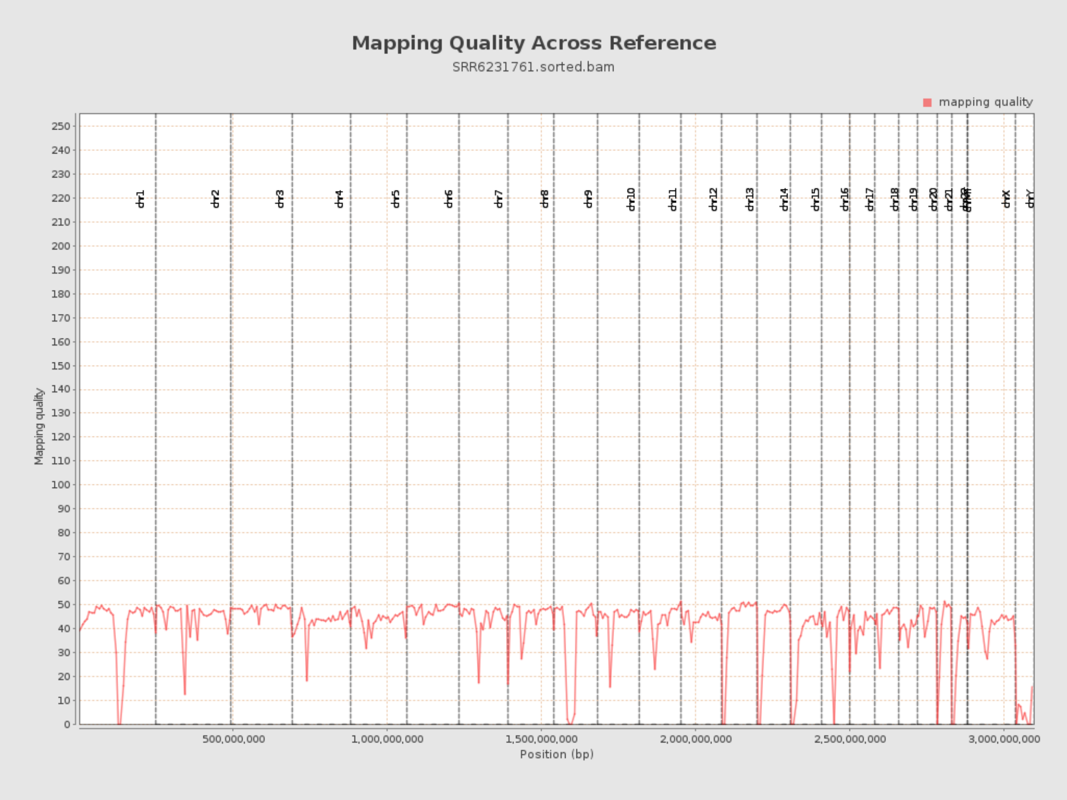
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram